

*Pst*I                      HCAYYY                      region CA                      HCA  
5' - GGAAACAAATTGAACATCATTCTATCAATACAACACAAACACAACACAACCTCAATCA  
acgtCCTTTGTTTTAAGTGTAGTAAGATAGTTATGTTGTGTTTGTGTTGTGTTGAGTTAGT  
  
YYY                      Nco I Xba I Sac I  
TTTATTGACAACACAACATAAACCAATGGTCTAGagct-3'  
AAATAAACTGTTGTGTTGATTTGTTGGTACCAGATC

Figure 3.

5'

← actin-1 rice → ← ubiquitin-1 corn →

ACCACCACCACCACCACCACCTCCTCCTTCACACAACACACACACAACAGATCTCCCCATCCT

← IVS2 → ← Bgl II →

CCCTCCCGTCGCGCCGCGCAACACCTGgtaagatggctgtgctgcgctcagatatatatagtgatat

← ubiquitin-1 corn →

gcactacaaagatcataactagaccgcgcctccccccccccccctctctaccttctctcttct

tttctccggttttttttttccgtctcgtctcgatctttggccttggtagtttgggggagagaggc

ggcttcgctcgcccagatcggtgcgcgttttttttatttggaggggaggatctcgcggtgggtc

← actin-1 rice →

tcggcgtgcggccggattctcgcggggaatggggctctcggatgtggatctgatccgccgttgt

tgggggagatatggggcggtttaaaatttcgccatgctaacaagatcaggaagaggggaaaagg

gcactatggtttaatttttatatatattctgtgctgctcgtcaggattagatgtgcttgatctt

tctttcttctttttgtgggtagaatttgaaatccctcagcattgttcacggtagtttttctttt

← ubiquitin-1 corn → ← IVS2 →

gtcgatgctcaccctgttgtttgggtgtttttatactagtggtatcctgacacgggtctctttgt

← Spe I →

caaatatctctgtgtgcagGTATAACTGCAGGAAACAACAATAACCATGG

← Pst I → ← Nco I → 3'

Figure 4.

box TATA transcription start  
ctatatataggaagttcatttcatttggagcccccaaccctACCACCACCACCACCACCT  
EXON  
CCTCCTTCACACAACACACACAACAGATCTCCCCATCCTCCCTCCCGTCGCGCCGCGCAAC  
Bgl II  
ACCTGgtaagatggctgtgcgctcagatatatatagtgatatgcactacaaagatcataactag  
intron  
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gggtgtttttataactagtggctatcctgacacggtctctttgtcaaatatctctgtgtgcagGTA  
Spe I  
TAACTGCAGGAAACAAATTGAACATCATTCTATCAATACAACACAAACACAACACAACACTCAATC  
Pst I EUREKA  
ATTTATTTGACAACACAACCTAAACAACCATGGTCTAGAGCTC  
Nco I Xba I Sac I

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Figure 5.

ATCCATAGCAAGCCCAGCCCAACCCAACCCAACCCACCCCAGTGCAGCCAACCTGGCAAA  
TAGTCTCCACACCCCGGCACTATCACCGTGAGTTGTCCGCACCACCGCACGTCTCGCAGCCAAA  
AAAAAAAAAAGAAAGAAAAAAAAAAGAAAAAGAAAAACAGCAGGTGGGTCCGGGTCTGTTGGGGGCC  
GGAAAAGCGAGGAGGATCGCGAGCAGCGACGAGGCCGGCCCTCCCTCCGCTTCCAAAGAAACGC  
*NruI*  
CCCCATCAATTctatatataggaagttcatttcatttggagccccccaaccctACCACCACCA  
CCACCACCACCTCCTCCTTCACACAACACACACACAACAGATCTCCCCATCCTCCCTCCCGTC  
*BglII*  
GCGCCGCGCAACACCTGgtaagatggctgtgcgctcagatatatatagtgatatgcactacaaa  
gatcataactagaccgcccctccccccccccccctctctaccttctctctttctttctcgtt  
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accctgttggttgggtgtttttatactagtggctatcctgacacggtctctttgtcaaatatctc  
*SpeI*  
tgtgtgcagGTATAACTGCAGGAAACAAATTGAACATCATTCTATCAATACAACACAAACACAA  
*PstI*  
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*Nco I Xba I Sac I*

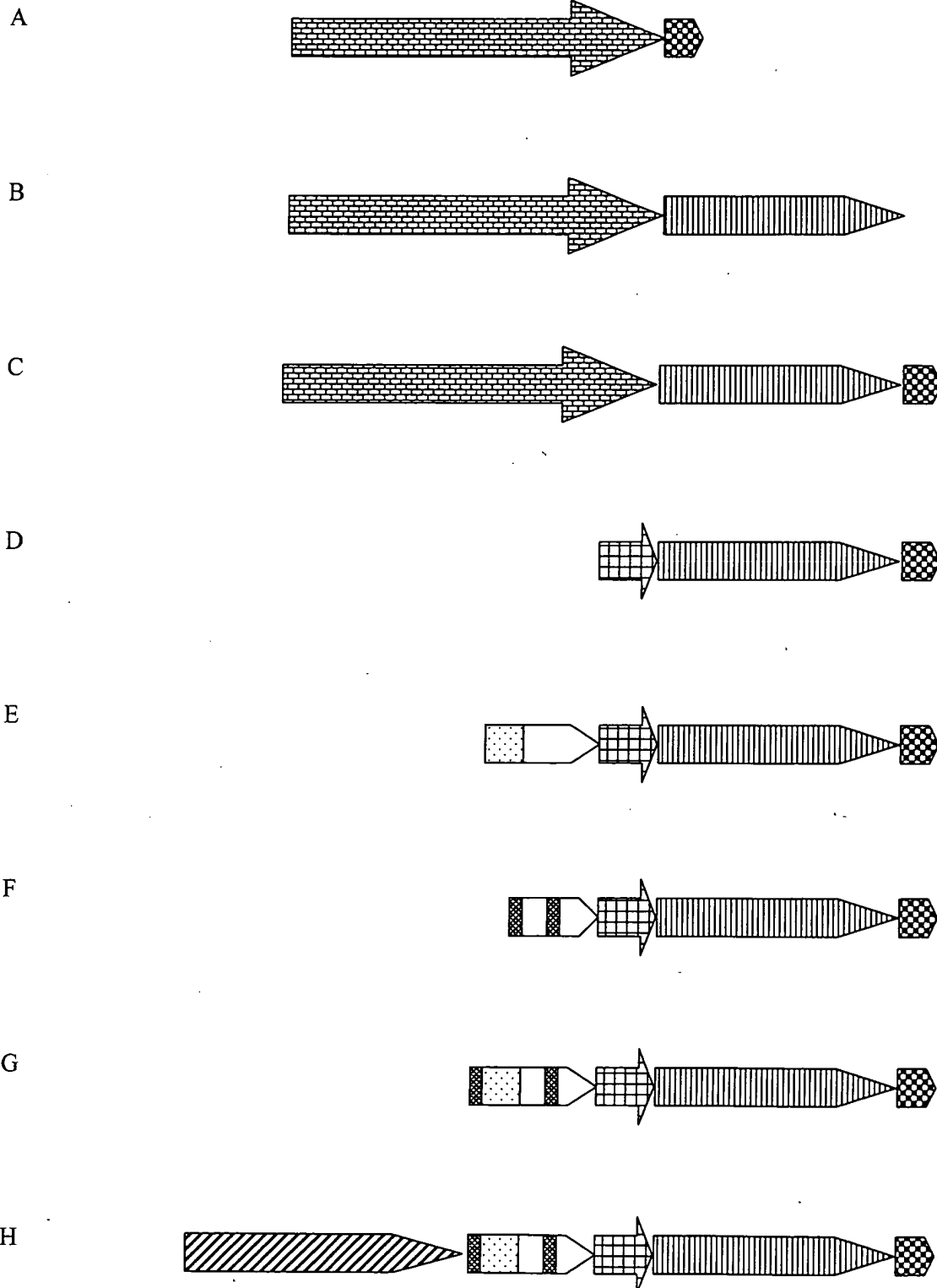
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Figure 6.

GGTACCGAGCATTGCATGTCTAAGTTATAAAAAATTACCACATATTTTTTTTGTACACTTGTT  
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TAGTACAACAATAATATCAGTGTTTTAGAGAATCATATAAATGAACAGTTAGACATGGTCTAAA  
GGACAATTGAGTATTTTGACAACAGGACTCTACAGTTTTATCTTTTTTAGTGTGCATGTGTTCTC  
CTTTTTTTTTTGCAAATAGCTTCACCTATATAATACTTCATCCATTTTATTAGTACATCCATTTA  
GGGTTTAGGGTTAATGGTTTTTATAGACTAATTTTTTTTAGTACATCTATTTTATTCTATTTTAG  
CCTCTAAATTAAGAAACTAAACTCTATTTTAGTTTTTTTTATTTAATAATTTAGATATAAAAT  
AGAATAAAATAAAGTGACTAAAAATTAAACAAATACCCTTTAAGAAATTAAAAAAACTAAGGAA  
ACATTTTTCTTGTTTTCGAGTAGATAATGCCAGCCTGTAAACGCCCTCGACT**GACGCTTCGAAT**  
**GACGCACATGCCATCCATAGCAAGCCCAGCCCAACCCAACCCAACCCAACCCACCCAGTGCAG**  
**CCA**ACTGGCAAATAGTCTCCACACCCCGGCACTATCACCGTGAGTTGTCCGCACCACCGCACGT  
CTCGCAGCCAAAAAAGAAAGAAAAAAGAAAAAGAAAAACAGCAGGTGGGTCCGG  
GTCGTGGGGGCCGAAAAGCGAGGAGGATCGCT**GACGCTTCGAATGACGCACATGCCCGAGCAG**  
CGACGAGGCCGGCCCTCCCTCCGCTTCCAAAGAAACGCCCCCATCAATTctatatataggaag  
ttcattttcatttgagagcccccaaccctaccaccaccaccaccaccacctcctccttcacacaa  
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Figure 7.



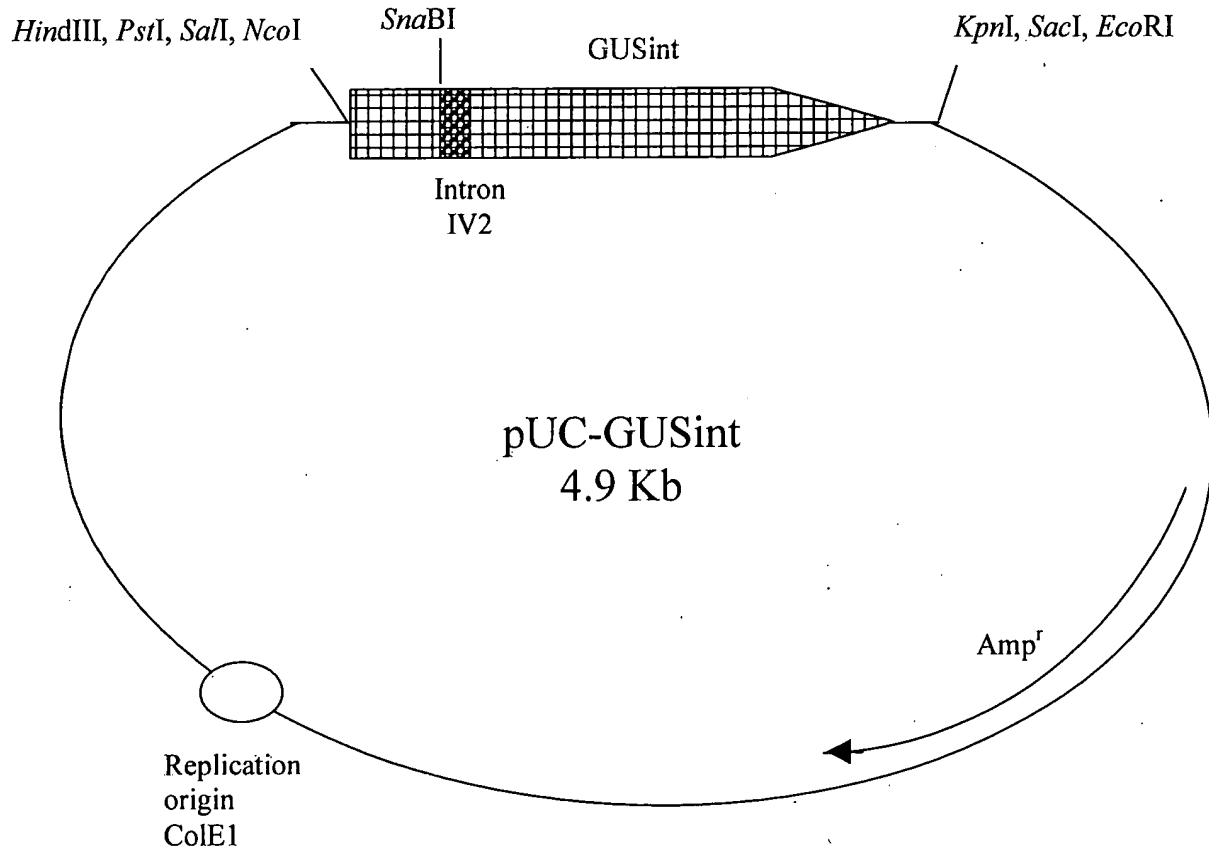
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Figure 8.

CTCGAGATACATATTAAGAGTATGGACAGACATTTCTTTAACAACTCCATTTGTATTACTCCA  
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TTCTTTTGTACTGTGTTTTAACACTACAAGCCATATATTGTCTGTACGTGCAACAACTATAT  
CACCATGTATCCCAAGATGCTTTTTTAATTtatatataggaagttcattttcatttggagcccc  
ccaaccctACCACCACCACCACCACCACCTCCTCCTTCACACAACACACACAACAGATCTCC  
CCCATCCTCCCTCCCGTCGCGCCGCGCAACACCTGgtaagatggctgtgcgctcagatatatat  
agtgatatgcactacaaagatcataactagaccgcccgcctccccccccccccctctctaccttc  
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TAGAGCTC Nco I  
*Xba I Sac I*

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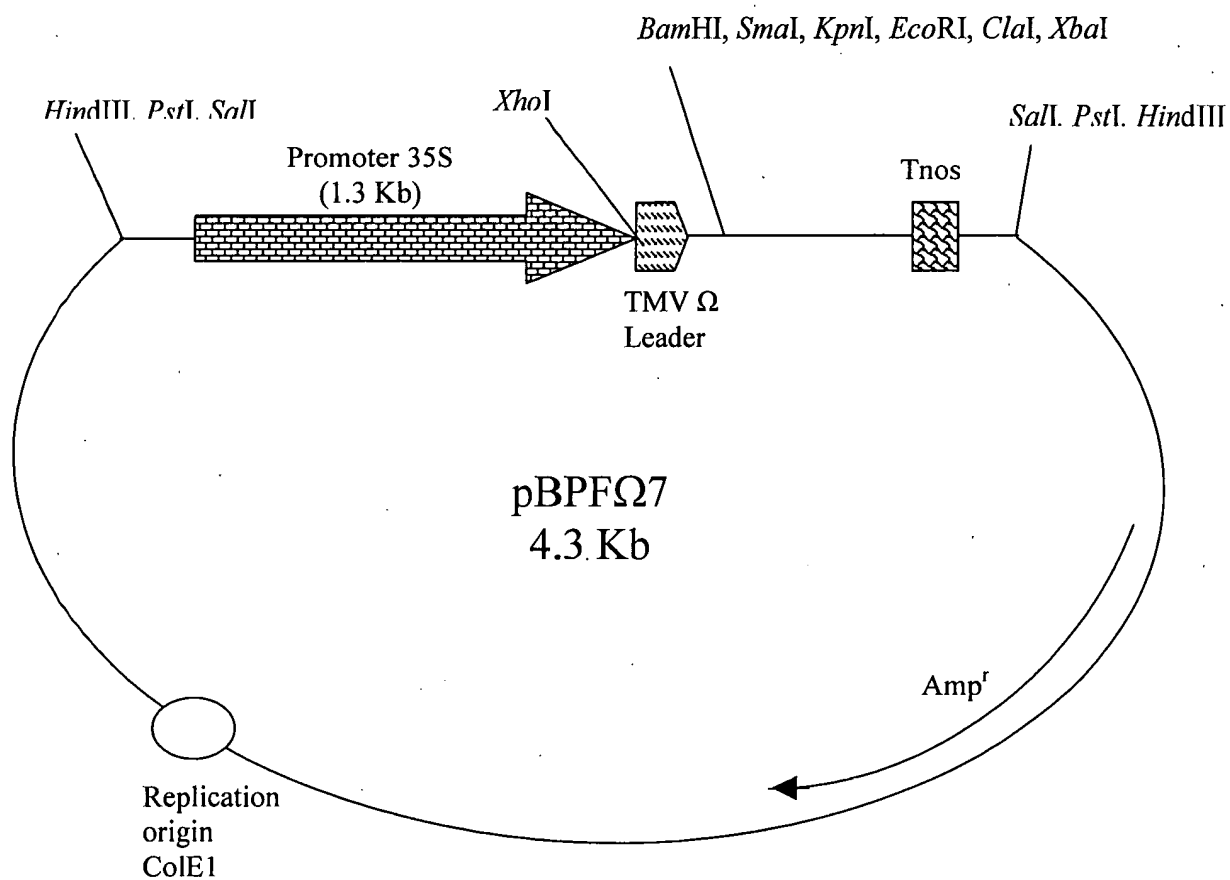
Figure 9.





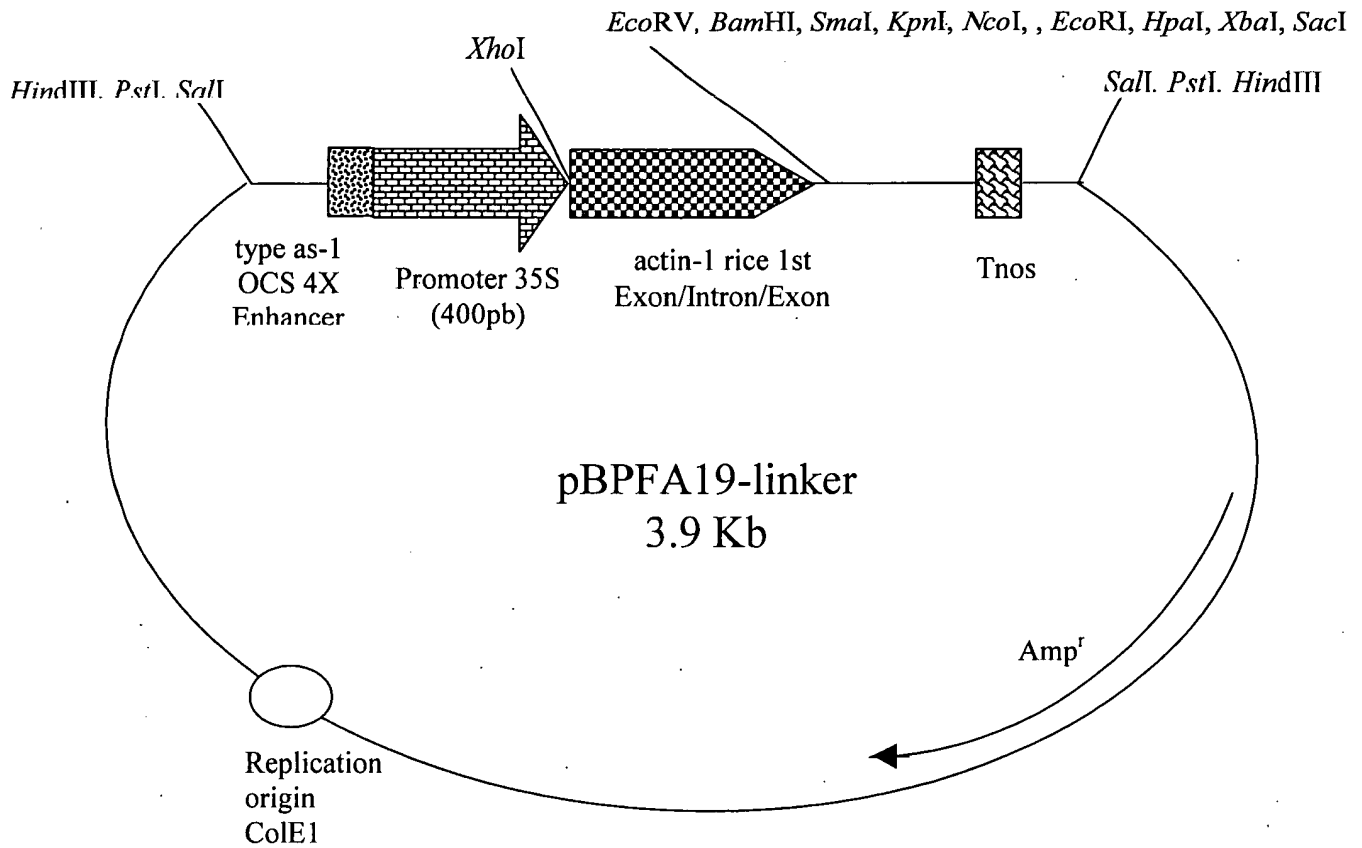
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Figure 10.



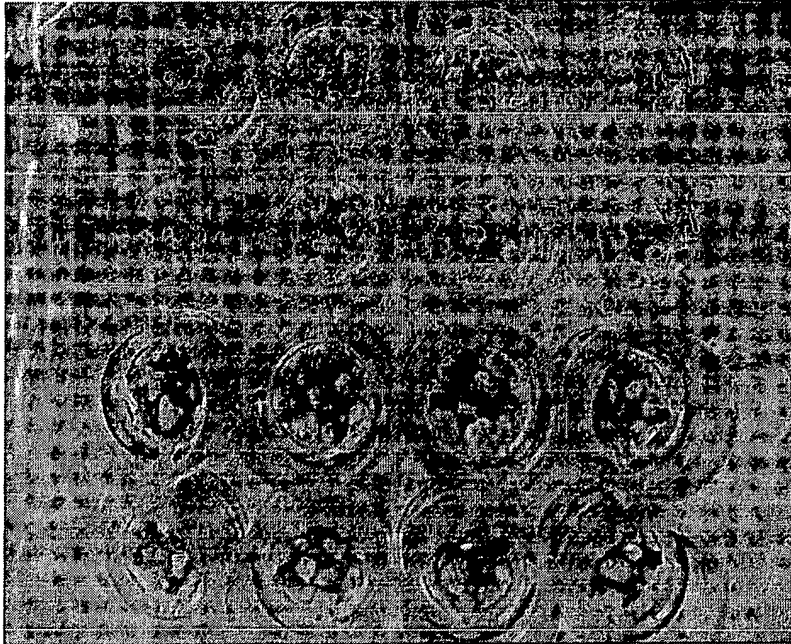
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Figure 11.



10/539476

Figure 12.



pBPFA19GUSint

pBPFΩ-GUSint

pA19ARTEGUSint

pA19ARTGUSint